It is also possible to use a smaller part (7 amino acids) of these 15 amino acids which lifts the neutralization of the virus by the monoclonal antibodies B1G6 or B2G2.2:

B1 cont.

04-R-7-V RTPKIQV (SEQ ID NO: 4) (Arg-Thr-Pro-Lys-Ile-Gln-Val)
05-S-7-K SQPKIVK (SEQ ID NO: 5) (Ser-Gln-Pro-Lys-Ile-Val-Lys)
06-F-7-E FHPSDIE (SEQ ID NO: 6) (Phe-His-Pro-Ser-Asp-Ile-Glu)

On pages 4 and 5, delete the bridging paragraph and replace this paragraph with the following in accordance with 37 CFR § 1.121. A marked up version showing changes is attached.

A common structure PKI (3 amino acids) appears to be the unit which is responsible; hence the following amino acid modifications:

07-TLSRTPKIQV (SEQ ID NO: 7) (Thr-Leu-Ser-Arg-Thr-Pro-Lys-Ile-Gln-Val) No. 185
08-IYLTQPKIKV (SEQ ID NO: 8) (Ile-Tyr-Leu-Thr-Gln-Pro-Lys-Ile-Lys-Val) No. 186

B2

09-IQRTPKIQVY (SEQ ID NO: 9) (Ile-Gln-Arg-Thr-Pro-Lys-Ile-Gln-Val-Tyr) No. 187
10-TLSQPKIVKN (SEQ ID NO: 10) (Thr-Leu-Ser-Gln-Pro-Lys-Ile-Val-Lys-Asn) No. 188
11-IQRTPQIVKW (SEQ ID NO: 11) (Ile-Gln-Arg-Thr-Pro-Gln-Ile-Val-Lys-Trp) No. 189
12-IQRTPNIVKW (SEQ ID NO: 12) (Ile-Gln-Arg-Thr-Pro-Asn-Ile-Val-Lys-Trp) No. 190

On page 5, delete the 1st, 2nd, and 3rd full paragraphs and replace these paragraphs with the following in accordance with 37 CFR § 1.121. A marked up version showing changes is attached.

B3

It is also possible to introduce a cysteine and a glycosylation site:

13-CYNPSDIE (SEQ ID NO: 13) (Cys-Tyr-Asn-Pro-Ser-Asp-Ile-Glu)

14-YCNPEST (SEQ ID NO: 14) (Tyr-Cys-Asn-Pro-Glu-Ser-Thr)

15-NFLNCYVS (SEQ ID NO: 15) (Asn-Phe-Leu-Asn-Cys-Tyr-Val-Ser)

16-LNCYVSPSD (SEQ ID NO: 16) (Leu-Asn-Cys-Tyr-Val-Ser-Pro-Ser-Asp)

Finally, it is possible to use the peptides using the different variations according to the species (mice, primates, rabbits, guinea pigs):

B3 Cont.

17-KTPQIQV (SEQ ID NO: 17) (Lys-Thr-Pro-Gln-Ile-Gln-Val)

18-FHPPQIE (SEQ ID NO: 18) (Phe-His-Pro-Pro-Gln-Ile-Glu)

19-FHPPHIE (SEQ ID NO: 19) (Phe-His-Pro-Pro-His-Ile-Glu)

20-AEPKTVY (SEQ ID NO: 20) (Ala-Glu-Pro-Lys-Thr-Val-Tyr)

21-SQPKTVY (SEQ ID NO: 21) (Ser-Gln-Pro-Lys-Thr-Val-Tyr)

22-ILSRTPKIQV (SEQ ID NO: 22) (Ile-Leu-Ser-Arg-Thr-Pro-Lys-Ile-Gln-Val)

These peptides of SEQ ID NOS. 1 to 22 contain only the preferential choice; it is possible, as has been indicated above, to find equivalent peptides.

On page 6, delete the 2nd full paragraph and replace this paragraph with the following in accordance with 37 CFR § 1.121. A marked up version showing changes is attached.

B4

Analysis of the structure of the regions selected for P1, P9 and P10 can be carried out by methods such as the selection using alanine to replace each amino acid separately, particularly in the RTPKIQV (SEQ ID NO: 4) region, in order to determine the possible amino acids. It is also possible to use techniques using biotinilation of each peptide, followed by selection by EIA with the antibodies in order to determine the loss of attachment.

On page 13, delete the 3rd full paragraph and replace this paragraph with the following in accordance with 37 CFR § 1.121. A marked up version showing changes is attached.

B5

The peptide R7V (RTPKIQV) (SEQ ID NO: 4) was extended by 2 amino acids in order to allow the coupling. The structure used as immunogen is RTPKIQVGY (SEQ ID NO: 23).

On pages 15-16, delete the bridging paragraph and replace this paragraph with the following in accordance with 37 CFR § 1.121. A marked up version showing changes is attached.

Methods

Chimeric recombinant viruses were constructed by PCR-directed mutagenesis. Two constructs based on the R7V sequence and HIV-1 LAV were obtained, in which seven amino acids of the V3 region of gpl2O have been replaced by the R7V sequence. The positions of the mutated sequences are shown in the following table: (SEQ ID NOS 24, 4 and 4, respectively in order of appearance).

B6

HIV-1 LAV (V3)	NNNTRKSIRIQRGPGRAFVT		
R7V	RTPKIQV	(1)	RPL
R7V	RTPKIQV	(2)	PLG

The $EcoRI_{52-78}$-$XhoI_{8401}$ fragment of HIV-1 LAV cloned into the vector Bluescript was used as template for subsequent constructs. In the first stage, the DNA fragments flanked by primers containing the BglII restriction site at one end and the nucleotide sequence encoding R7V at the other end were synthesized for the RPL and PLG constructs by PCR amplification. The mutagenesis oligonucleotides used consisted of a (+) primer ACACCAAAGATACAAGTTGTTACAAATAGGAAAA (SEQ ID NO: 25) and a (-) primer TTGTATCTTTGGTGTTCTCTGGATCCGGATACTTT (SEQ ID NO: 26) for the RPL construct and of a (+) primer CGTACACCAAAAATCCAGGTCCAGAGAGGACCA (SEQ ID NO: 27) and a (-) primer GATTTTTGGTGTACGCGTATTGTTGTTGGGTCT (SEQ ID NO: 28) for the PLG construct. In the second stage, two PCR products for each construct were mixed and amplified using the primers containing the BglII restriction sites. The RPL and PLG fragments were cleaved by the enzyme BglII and inserted into the vector Bluescript containing the $EcoRI_{5278}$-$XhoI_{8401}$ fragment of HIV-1 LAV, cleaved by BglII. In addition to the R7V sequence, the amplification primers contained modifications in the nucleotide sequence leading to the appearance of new BamHI and MluI restriction sites in the RPL and PLG constructs respectively, without additional modifications in the amino acid sequence. The new restriction sites were used to screen the mutated sequences. Finally, the $EcoRI_{5278}$-$XhoI_{8401}$ fragments of HIV-1 LAV containing the RPL and PLG constructs were inserted into the plasmid pNL4-3 by